



Warf Sequence.ST25.txt
SEQUENCE LISTING

<110> Harms, Jerome S
Splitter, Gary A
Eakle, Kurt A
Bremel, Robert D

<120> Inducible Protein Expression System

<130> 2240/3

<140> US 10/763,976

<141> 2004-01-23

<160> 65

<170> PatentIn version 3.3

<210> 1

<211> 576

<212> DNA

<213> Artificial

<220>

<223> Engineered Sequence from virus and plasmid

<220>

<221> Promoter

<222> (87)..(432)

<223> BLV Promoter

<400> 1

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aattacaact gctagaaaat gaatggctct cccgcctttt ttgaggggga atcatttgta      180
tgaaagatca tgccgaccta ggcgccgcca ccgccccgta aaccagacag agacgtcagc      240
tgccagaaaa gctggtgacg gcagctggtg gctagaatcc ccgtacctcc ccaacttccc      300
ctttcccgaa aaatccacac cctgagctgc tgacctcacc tgctgataaa ttaataaaat      360
gccggccctg tcgagttagc ggcaccagaa gcgttcttct cctgagaccc tcgtgctcag      420
ctctcggtcc tgcctcgaga agcttggtat cacaagtttg tacaaaaaag ctgaacgaga      480
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ataatactgt aaaacacaac atatccagtc actatg      576
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<210> 2

<211> 930

<212> DNA

<213> Bovine leukemia virus

<220>

<221> CDS

<222> (1)..(930)

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<400> 2
atg gca agt gtt gtt ggt tgg ggg ccc cac tct cta cat gcc tgc ccg      48
Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys Pro
1 5 10 15

gcc ctg gtt ttg tcc aat gac gtc acc atc gat gcc tgg tgc ccc ctc      96
Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
20 25 30

tgc ggg ccc cat gag cga ctc caa ttc gaa agg atc gac acc acg cac      144
Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr His
35 40 45

acc tgc gag acc cac cgt atc acc tgg acc gcc gat gga cga cct ttc      192
Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp Gly Arg Pro Phe
50 55 60

ggc ctc aat gga gcg ctg ttc cct cga ctg cat gtc tcc aga gac ccg      240
Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His Val Ser Arg Asp Pro
65 70 75 80

gcc cca agg gcc cga cga ctc tgg atc aac tgc ccc ctt ccg gcc gtt      288
Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
85 90 95

cgc gct cag ccc ggc ccg gtt tca ctt tcc ccc ttc gag cgg tcc ccc      336
Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
100 105 110

ttc cag ccc tac caa tgc caa ttg ccc tcg gcc tct agc gac ggt tgc      384
Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
115 120 125

ccc gtc atc ggg cac ggc ctt ctt ccc tgg aac aac tta gta acg cat      432
Pro Val Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
130 135 140

cct tgt cct cgg aaa gtc ctt ata tta aat caa atg gcc aat ttt tcc      480
Pro Cys Pro Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
145 150 155 160

tta ctc ccc ccc ttc aat acc ctc ctt gtg gac ccc ctc cgg ttg tcc      528
Leu Leu Pro Pro Phe Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
165 170 175

gtc ttt gcc cca gac acc agg gga gcc ata cgt tat ctc tcc acc ctt      576
Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
180 185 190

ttg acg cta tgc cca gct act tgt att cta ccc ctc ggc gag ccc ttc      624
Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
195 200 205

tct cct aat gtc ccc ata tgt cgc ttt ccc cgg gac tcc aat gaa ccc      672
Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
210 215 220

ccc ctt tca gaa ttc gag ctg ccc ctt atc caa acg ccc ggc ctg tct      720
Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
225 230 235 240

tgg tct gtc ccc gcg atc gac cta ttc cta acc ggc ccc cct tcc cca      768

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Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
245 250 255

tgc gac cgg tta cac gta tgg tcc agt cct cag gcc tta cag cgc ttc 816
Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
260 265 270

ctc cat gac cct acg cta acc tgg tca gaa ttg gtt gct agc agg aaa 864
Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
275 280 285

cta aga ctt gat tca ccc tta aaa tta caa ctg tta gaa aat gaa tgg 912
Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp
290 295 300

ctc tcc cgc ctt ttt tga 930
Leu Ser Arg Leu Phe
305

<210> 3
<211> 309
<212> PRT
<213> Bovine leukemia virus

<400> 3

Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys Pro
1 5 10 15

Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
20 25 30

Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr His
35 40 45

Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp Gly Arg Pro Phe
50 55 60

Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His Val Ser Arg Asp Pro
65 70 75 80

Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
85 90 95

Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
100 105 110

Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
115 120 125

Pro Val Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
130 135 140

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Pro Cys Pro Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
145 150 155 160

Leu Leu Pro Pro Phe Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
165 170 175

Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
180 185 190

Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
195 200 205

Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
210 215 220

Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
225 230 235 240

Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
245 250 255

Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
260 265 270

Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
275 280 285

Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp
290 295 300

Leu Ser Arg Leu Phe
305

<210> 4
<211> 1062
<212> DNA
<213> Human T-cell lymphotropic virus type 1

<220>
<221> promoter
<222> (1)..(353)

<400> 4
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ggagacggcg actggtgccc ctgtgtacaa atctctgggg gactatgttc ggcccgcta 120
catcgtcacg ccctactggc cacctgtcca gagcatcaga tcacctggga ccccatcgat 180
ggacgcgtta tcggctcagc tctacagttc cttatccctc gactccctc cttccccacc 240

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cagagaacct ctaagaccct caaggctcctt accccgccaa tcactcatac aaccccccaac 300
attccaccct ccttcctcca ggccatgcmc aaatactccc ccttccgaaa tggatacatg 360
gaaccacccc ttgggcagca cctcccaacc ctgtcttttc cagaccccgg actccggccc 420
caaaacctgt acaccctctg gggaggctcc gttgtctgca tgtacctcta ccagcttttc 480
ccccccatca cctggcccct cctgccccac gtgatttttt gccaccccgg ccagctcggg 540
gccttctca ccaatgttcc ctacaagcga atagaagaac tcctctataa aatttcctt 600
accacagggg ccctaataat tctaccgaa gactgtttgc ccaccaccct tttccagcct 660
gttagggcac ccgtcacgct aacagcctgg caaaacggcc tccttccgtt ccactcaacc 720
ctcaccactc caggccttat ttggacattt accgatggca cgcctatgat ttccggggcc 780
tgccctaaag atggccagcc atctttagta ctacagtcct cctcctttat atttcacaaa 840
tttcaaacca aggcctacca cccctcattt ctactctcac acggcctcat acagtactct 900
tcctttcata atttacatct cctgtttgaa gaatacacca acatcccat ttctctactt 960
tttaacaaaa aagaggcaga tgacaatgac catgagcccc aaatatcccc cgggggctta 1020
gagcctccca gtgaaaaaca tttccgcgaa acagaagtct ga 1062

<210> 5
<211> 353
<212> DNA
<213> Human T-cell lymphotropic virus type 1

<400> 5
tgacaatgac catgagcccc aaatatcccc cgggggctta gagcctctca gtgaaaaaca 60
tttccgtgaa acagaagtct gagaaggctca gggcccagaa taaggctctg acgtctcccc 120
ccggaggaca gctcagcacc agctcaggct aggccttgac gtgtccccct aaagacaaat 180
cataagctca gacctccggg aagccaccgg gaaccaccca tttcctcccc atgtttgtca 240
agccgtcctc aggcgttgac gacaaccct cactcaaaa aacttttcat ggcacgcata 300
cggctcaata aaataacagg agtctataaa agcgtgggga cagttcagga ggg 353

<210> 6
<211> 456
<212> DNA
<213> Human immunodeficiency virus type 1

<220>
<221> CDS
<222> (1)..(456)

<400> 6
ctg gaa ggg cta att tgg tcc caa aga aga caa gag atc ctt gat ctg 48
Leu Glu Gly Leu Ile Trp Ser Gln Arg Arg Gln Glu Ile Leu Asp Leu
1 5 10 15

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tgg atc tac cac aca caa ggc tac ttc cct gat tgg cag aat tac aca	96
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr	
20 25 30	
cca ggg cca ggg atc aga tat cca ctg acc ttt gga tgg tgc ttc aag	144
Pro Gly Pro Gly Ile Arg Tyr Pro Leu Thr Phe Gly Trp Cys Phe Lys	
35 40 45	
cta gta cca gtt gag cca gag aag gta gaa gag gcc aat gaa gga gag	192
Leu Val Pro Val Glu Pro Glu Lys Val Glu Glu Ala Asn Glu Gly Glu	
50 55 60	
aac aac agc ttg tta cac cct atg agc ctg cat ggg atg gag gac gcg	240
Asn Asn Ser Leu Leu His Pro Met Ser Leu His Gly Met Glu Asp Ala	
65 70 75 80	
gag aaa gaa gtg tta gtg tgg agg ttt gac agc aaa cta gca ttt cat	288
Glu Lys Glu Val Leu Val Trp Arg Phe Asp Ser Lys Leu Ala Phe His	
85 90 95	
cac atg gcc cga gag ctg cat ccg gag tac tac aaa gac tgc tga cat	336
His Met Ala Arg Glu Leu His Pro Glu Tyr Tyr Lys Asp Cys His	
100 105 110	
cga gct ttc tac aag gga ctt tcc gct ggg gac ttt cca ggg agg cgt	384
Arg Ala Phe Tyr Lys Gly Leu Ser Ala Gly Asp Phe Pro Gly Arg Arg	
115 120 125	
ggc ctg ggc ggg act ggg gag tgg cgt ccc tca gat gct gca tat aag	432
Gly Leu Gly Gly Thr Gly Glu Trp Arg Pro Ser Asp Ala Ala Tyr Lys	
130 135 140	
cag ctg ctt ttt gcc tgt act ggg	456
Gln Leu Leu Phe Ala Cys Thr Gly	
145 150	

<210> 7
 <211> 110
 <212> PRT
 <213> Human immunodeficiency virus type 1

<400> 7

Leu Glu Gly Leu Ile Trp Ser Gln Arg Arg Gln Glu Ile Leu Asp Leu
 1 5 10 15

Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
 20 25 30

Pro Gly Pro Gly Ile Arg Tyr Pro Leu Thr Phe Gly Trp Cys Phe Lys
 35 40 45

Leu Val Pro Val Glu Pro Glu Lys Val Glu Glu Ala Asn Glu Gly Glu
 50 55 60

Asn Asn Ser Leu Leu His Pro Met Ser Leu His Gly Met Glu Asp Ala
 65 70 75 80

warf Sequence.ST25.txt

Glu Lys Glu Val Leu Val Trp Arg Phe Asp Ser Lys Leu Ala Phe His
85 90 95

His Met Ala Arg Glu Leu His Pro Glu Tyr Tyr Lys Asp Cys
100 105 110

<210> 8
<211> 41
<212> PRT
<213> Human immunodeficiency virus type 1

<400> 8

His Arg Ala Phe Tyr Lys Gly Leu Ser Ala Gly Asp Phe Pro Gly Arg
1 5 10 15

Arg Gly Leu Gly Gly Thr Gly Glu Trp Arg Pro Ser Asp Ala Ala Tyr
20 25 30

Lys Gln Leu Leu Phe Ala Cys Thr Gly
35 40

<210> 9
<211> 306
<212> DNA
<213> Human immunodeficiency virus type 1

<220>
<221> CDS
<222> (1)..(303)

<400> 9

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Met Glu Pro Val Asp Pro Asn Leu Glu Pro Trp Lys His Pro Gly Ser
1 5 10 15

cag cct agg act gct tgt aac aat tgc tat tgt aaa aag tgt tgc ttt 96
Gln Pro Arg Thr Ala Cys Asn Asn Cys Tyr Cys Lys Lys Cys Cys Phe
20 25 30

cat tgc tac gcg tgt ttc aca aga aaa ggc tta ggc atc tcc tat ggc 144
His Cys Tyr Ala Cys Phe Thr Arg Lys Gly Leu Gly Ile Ser Tyr Gly
35 40 45

agg aag aag cgg aga cag cga aga gct cct cag gac agt cag act 192
Arg Lys Lys Arg Arg Gln Arg Arg Ala Pro Gln Asp Ser Gln Thr
50 55 60

cat caa gct tct cta tca aag caa ccc gcc tcc cag tcc cga ggg gac 240
His Gln Ala Ser Leu Ser Lys Gln Pro Ala Ser Gln Ser Arg Gly Asp
65 70 75 80

ccg aca ggc ccg acg gaa tcg aag aag aag gtg gag aga gag aca gag 288
Pro Thr Gly Pro Thr Glu Ser Lys Lys Lys Val Glu Arg Glu Thr Glu
85 90 95

aca gat ccg ttc gat tag
 Thr Asp Pro Phe Asp
 100

<210> 10
 <211> 101
 <212> PRT
 <213> Human immunodeficiency virus type 1
 <400> 10

Met Glu Pro Val Asp Pro Asn Leu Glu Pro Trp Lys His Pro Gly Ser
 1 5 10 15

Gln Pro Arg Thr Ala Cys Asn Asn Cys Tyr Cys Lys Lys Cys Cys Phe
 20 25 30

His Cys Tyr Ala Cys Phe Thr Arg Lys Gly Leu Gly Ile Ser Tyr Gly
 35 40 45

Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro Gln Asp Ser Gln Thr
 50 55 60

His Gln Ala Ser Leu Ser Lys Gln Pro Ala Ser Gln Ser Arg Gly Asp
 65 70 75 80

Pro Thr Gly Pro Thr Glu Ser Lys Lys Lys Val Glu Arg Glu Thr Glu
 85 90 95

Thr Asp Pro Phe Asp
 100

<210> 11
 <211> 309
 <212> PRT
 <213> Bovine leukemia virus
 <400> 11

Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys Pro
 1 5 10 15

Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
 20 25 30

Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr His
 35 40 45

Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp Gly Arg Pro Phe
 50 55 60

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Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His Val Ser Arg Asp Pro
65 70 75 80

Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
85 90 95

Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
100 105 110

Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
115 120 125

Pro Val Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
130 135 140

Pro Cys Pro Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
145 150 155 160

Leu Leu Pro Pro Phe Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
165 170 175

Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
180 185 190

Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
195 200 205

Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
210 215 220

Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
225 230 235 240

Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
245 250 255

Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
260 265 270

Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
275 280 285

Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp
290 295 300

Leu Ser Arg Leu Phe
305

warf Sequence.ST25.txt

<210> 12
 <211> 353
 <212> PRT
 <213> Human T-cell lymphotropic virus type 1

<400> 12

Met Ala His Phe Pro Gly Phe Gly Gln Ser Leu Leu Phe Gly Tyr Pro
 1 5 10 15

Val Tyr Val Phe Gly Asp Cys Val Gln Gly Asp Trp Cys Pro Ile Ser
 20 25 30

Gly Gly Leu Cys Ser Ala Arg Leu His Arg His Ala Leu Leu Ala Thr
 35 40 45

Cys Pro Glu His Gln Ile Thr Trp Asp Pro Ile Asp Gly Arg Val Ile
 50 55 60

Gly Ser Ala Leu Gln Phe Leu Ile Pro Arg Leu Pro Ser Phe Pro Thr
 65 70 75 80

Gln Arg Thr Ser Lys Thr Leu Lys Val Leu Thr Pro Pro Ile Thr His
 85 90 95

Thr Thr Pro Asn Ile Pro Pro Ser Phe Leu Gln Ala Met Arg Lys Tyr
 100 105 110

Ser Pro Phe Arg Asn Gly Tyr Met Glu Pro Thr Leu Gly Gln His Leu
 115 120 125

Pro Thr Leu Ser Phe Pro Asp Pro Gly Leu Arg Pro Gln Asn Leu Tyr
 130 135 140

Thr Leu Trp Gly Gly Ser Val Val Cys Met Tyr Leu Tyr Gln Leu Ser
 145 150 155 160

Pro Pro Ile Thr Trp Pro Leu Leu Pro His Val Ile Phe Cys His Pro
 165 170 175

Gly Gln Leu Gly Ala Phe Leu Thr Asn Val Pro Tyr Lys Arg Ile Glu
 180 185 190

Glu Leu Leu Tyr Lys Ile Ser Leu Thr Thr Gly Ala Leu Ile Ile Leu
 195 200 205

Pro Glu Asp Cys Leu Pro Thr Thr Leu Phe Gln Pro Val Arg Ala Pro
 210 215 220

warf Sequence.ST25.txt

Val Thr Leu Thr Ala Trp Gln Asn Gly Leu Leu Pro Phe His Ser Thr
225 230 235 240

Leu Thr Thr Pro Gly Leu Ile Trp Thr Phe Thr Asp Gly Thr Pro Met
245 250 255

Ile Ser Gly Pro Cys Pro Lys Asp Gly Gln Pro Ser Leu Val Leu Gln
260 265 270

Ser Ser Ser Phe Ile Phe His Lys Phe Gln Thr Lys Ala Tyr His Pro
275 280 285

Ser Phe Leu Leu Ser His Gly Leu Ile Gln Tyr Ser Ser Phe His Asn
290 295 300

Leu His Leu Leu Phe Glu Glu Tyr Thr Asn Ile Pro Ile Ser Leu Leu
305 310 315 320

Phe Asn Lys Lys Glu Ala Asp Asp Asn Asp His Glu Pro Gln Ile Ser
325 330 335

Pro Gly Gly Leu Glu Pro Pro Ser Glu Lys His Phe Arg Glu Thr Glu
340 345 350

Val

<210> 13
<211> 101
<212> PRT
<213> Human T-cell lymphotropic virus type 1
<400> 13

Met Glu Pro Val Asp Pro Asn Leu Glu Pro Trp Lys His Pro Gly Ser
1 5 10 15

Gln Pro Arg Thr Ala Cys Asn Asn Cys Tyr Cys Lys Lys Cys Cys Phe
20 25 30

His Cys Tyr Ala Cys Phe Thr Arg Lys Gly Leu Gly Ile Ser Tyr Gly
35 40 45

Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro Gln Asp Ser Gln Thr
50 55 60

His Gln Ala Ser Leu Ser Lys Gln Pro Ala Ser Gln Ser Arg Gly Asp
65 70 75 80

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Pro Thr Gly Pro Thr Glu Ser Lys Lys Lys Val Glu Arg Glu Thr Glu
85 90 95

Thr Asp Pro Phe Asp
100

<210> 14
<211> 7685
<212> DNA
<213> Artificial

<220>
<223> Engineered Sequence from virus and plasmid

<220>
<221> LTR
<222> (149)..(737)
<223> 5' MoMuSVLTR

<220>
<221> CDS
<222> (1753)..(2148)
<223> Blasticidin Resistance

<220>
<221> promoter
<222> (2257)..(3074)
<223> CMV IE promoter

<220>
<221> misc_recomb
<222> (3078)..(3102)
<223> attB1

<220>
<221> CDS
<222> (3115)..(4041)
<223> BLV Tax

<220>
<221> misc_recomb
<222> (4046)..(4070)
<223> attB2

<220>
<221> misc_signal
<222> (4082)..(4674)
<223> WPRE; woodchuck hepatitis virus post-transcriptional regulatory element

<220>
<221> LTR
<222> (4720)..(5313)
<223> 3' MoMuLVLTR

<220>
<221> CDS
<222> (6616)..(7476)
<223> Ampicillin Resistance

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<400> 14
gaattaattc ataccagatc accgaaaact gtcctccaaa tgtgtccccc tcacactccc      60
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aaagccgcgg cccttccggt tctttgcttt tgaaagaccc cacccgtagg tggcaagcta      180
gcttaagtaa cgccactttg caaggcatgg aaaaatacat aactgagaat agaaaagttc      240
agatcaaggt caggaacaaa gaaacagctg aataccaaac aggatatctg tggtaagcgg      300
ttcctgcccc ggctcagggc caagaacaga tgagacagct gagtgatggg ccaaacagga      360
tatctgtggg aagcagttcc tgccccggct cggggccaag aacagatggg cccagatgc      420
gggtccagccc tcagcagttt ctagtgaatc atcagatggt tccaggggtgc cccaaggacc      480
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cttccgatag actgcgtcgc ccgggtaccc gtattcccaa taaagcctct tgctgtttgc      660
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gacgggggtc tttcatttgg gggctcgtcc gggatttggg gacccctgcc cagggaccac      780
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cgtctgaatt tttgctttcg gtttggaaac gaagccgcgc gtcttgtctg ctgcagcgt      1140
gcagcatcgt tctgtgttgt ctctgtctga ctgtgtttct gtatttgtct gaaaattagg     1200
gccagactgt taccactccc ttaagtttga ccttaggtca ctggaaagat gtcgagcggg     1260
tcgctcaca ccagtcggtg gatgtcaaga agagacgttg ggttaccttc tgctctgcag     1320
aatggccaac ctttaacgtc ggatggccgc gagacggcac ctttaaccga gacctcatca     1380
cccagggtta gatcaaggtc tttcacctg gcccgcgtgg acaccagac cagggtcccct     1440
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accctaagcc tccgcctcct ctccctccat ccgccccgtc tctccccctt gaacctcctc     1560
gttcgacccc gcctcgatcc tccctttatc cagccctcac tccttctcta ggcgccggaa     1620
ttccgatctg atcaagagac aggatgaggg agcttgata tccattttcg gatctgatca     1680
gcacgtgttg acaattaatc atcggcatag tatatcggca tagtataata cgacaaggtg     1740
aggaactaaa cc atg gcc aag cct ttg tct caa gaa gaa tcc acc ctc att     1791
          1      5      10
Met Ala Lys Pro Leu Ser Gln Glu Glu Ser Thr Leu Ile

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gaa aga gca acg gct aca atc aac agc atc ccc atc tct gaa gac tac Glu Arg Ala Thr Ala Thr Ile Asn Ser Ile Pro Ile Ser Glu Asp Tyr 15 20 25	1839
agc gtc gcc agc gca gct ctc tct agc gac ggc cgc atc ttc act ggt Ser Val Ala Ser Ala Ala Leu Ser Ser Asp Gly Arg Ile Phe Thr Gly 30 35 40 45	1887
gtc aat gta tat cat ttt act ggg gga cct tgt gca gaa ctc gtg gtg Val Asn Val Tyr His Phe Thr Gly Gly Pro Cys Ala Glu Leu Val Val 50 55 60	1935
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gcg atc gga aat gag aac agg ggc atc ttg agc ccc tgc gga cgg tgt Ala Ile Gly Asn Glu Asn Arg Gly Ile Leu Ser Pro Cys Gly Arg Cys 80 85 90	2031
cga cag gtg ctt ctc gat ctg cat cct ggg atc aaa gcg ata gtg aag Arg Gln Val Leu Leu Asp Leu His Pro Gly Ile Lys Ala Ile Val Lys 95 100 105	2079
gac agt gat gga cag ccg acg gca gtt ggg att cgt gaa ttg ctg ccc Asp Ser Asp Gly Gln Pro Thr Ala Val Gly Ile Arg Glu Leu Leu Pro 110 115 120 125	2127
tct ggt tat gtg tgg gag ggc taagcacttc gtggccgagg agcaggactg Ser Gly Tyr Val Trp Glu Gly 130	2178
acacgtgcta cgagatttcg attccaccgc cgccttctat gaaaggttgg gcttcggaat	2238
cgttttccgg gacgccgatc cggccattag ccatattatt cattggttat atagcataaa	2298
tcaatattgg ctattggcca ttgcatacgt tgtatccata tcataatatg tacatttata	2358
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gtcgtaaaca ctccgcccc ttgacgcaaa tgggcggtag gcatgtacgg tgggaggtct	2958
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Warf Sequence.ST25.txt

caagttt	tgta	caaaaa	agca	ggctccc	gcc	cacc	atg	gca	agt	ggt	ggt	ggt				3132
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Trp	Gly	Pro	His	Ser	Leu	His	Ala	Cys	Pro	Ala	Leu	Val	Leu	Ser	Asn	
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145																
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Asp	Val	Thr	Ile	Asp	Ala	Trp	Cys	Pro	Leu	Cys	Gly	Pro	His	Glu	Arg	
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170																
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185																
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225																
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235																
240																
245																
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caa	ttg	ccc	tgc	gcc	tct	agc	gac	ggc	tgc	ccc	att	atc	ggg	cac	ggc	3516
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Leu	Leu	Pro	Trp	Asn	Asn	Leu	Val	Thr	His	Pro	Val	Leu	Arg	Lys	Val	
270																
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ctt	ata	tta	aat	caa	atg	gcc	aat	ttt	tcc	tta	ctc	ccc	tcc	ttc	gat	3612
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Thr	Leu	Leu	Val	Asp	Pro	Leu	Arg	Leu	Ser	Val	Phe	Ala	Pro	Asp	Thr	
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310																
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Arg	Gly	Ala	Ile	Arg	Tyr	Leu	Ser	Thr	Leu	Leu	Thr	Leu	Cys	Pro	Ala	
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325																
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act	tgt	att	cta	ccc	cta	ggc	gag	ccc	ttc	tct	cct	aat	gtc	ccc	ata	3756
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340																
345																
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Cys	Arg	Phe	Pro	Arg	Asp	Ser	Asn	Glu	Pro	Pro	Leu	Ser	Glu	Phe	Glu	
350																
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360																
ctg	ccc	ctt	atc	caa	acg	ccc	ggc	ctg	tct	tgg	tct	gtc	ccc	gcg	atc	3852
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370																
375																

warf Sequence.ST25.txt

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tgg tcc agt cct cag gcc tta cag cgc ttc ctt cat gac cct acg cta Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe Leu His Asp Pro Thr Leu 395 400 405 410	3948
acc tgg tcc gaa tta gtt gct agc aga aaa ata aga ctt gat tcc ccc Thr Trp Ser Glu Leu Val Ala Ser Arg Lys Ile Arg Leu Asp Ser Pro 415 420 425	3996
tta aaa tta caa ctg cta gaa aat gaa tgg ctc tcc cgc ctt ttt Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp Leu Ser Arg Leu Phe 430 435 440	4041
tgagacccag ctttcttgta caaagtgggtg ataacatcga taatcaacct ctggattaca	4101
aaattttgtga aagattgact ggtattctta actatgttgc tcctttttacg ctatgtggat	4161
acgctgcttt aatgcctttg tatcatgcta ttgcttcccg tatggctttc attttctcct	4221
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Warf Sequence.ST25.txt

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ccgcatcagg cgctcttccg ctctctcgct cactgactcg ctgcgctcgg tcgttcggct 5721
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Leu

cca atg ctt aat cag tga ggc acc tat ctc agc gat ctg tct att tcg 6666
Pro Met Leu Asn Gln Gly Thr Tyr Leu Ser Asp Leu Ser Ile Ser
445 450 455

ttc atc cat agt tgc ctg act ccc cgt cgt gta gat aac tac gat acg 6714
Phe Ile His Ser Cys Leu Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr
460 465 470

gga ggg ctt acc atc tgg ccc cag tgc tgc aat gat acc gcg aga ccc 6762
Gly Gly Leu Thr Ile Trp Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro
475 480 485

acg ctc acc ggc tcc aga ttt atc agc aat aaa cca gcc agc cgg aag 6810
Thr Leu Thr Gly Ser Arg Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys
490 495 500 505

ggc cga gcg cag aag tgg tcc tgc aac ttt atc cgc ctc cat cca gtc 6858
Gly Arg Ala Gln Lys Trp Ser Cys Asn Phe Ile Arg Leu His Pro Val
510 515 520

tat taa ttg ttg ccg gga agc tag agt aag tag ttc gcc agt taa tag 6906

Warf Sequence.ST25.txt

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Phe	Ala	Gln	Arg	Cys	Cys	His	Cys	Cys	Arg	His	Arg	Gly	Val	Thr	Leu	
		535					540					545				
gtc	ggt	tgg	tat	ggc	ttc	att	cag	ctc	cgg	ttc	cca	acg	atc	aag	gcg	7002
Val	Val	Trp	Tyr	Gly	Phe	Ile	Gln	Leu	Arg	Phe	Pro	Thr	Ile	Lys	Ala	
		550				555					560					
agt	tac	atg	atc	ccc	cat	ggt	gtg	caa	aaa	agc	ggt	tag	ctc	ctt	cgg	7050
Ser	Tyr	Met	Ile	Pro	His	Val	Val	Gln	Lys	Ser	Gly		Leu	Leu	Arg	
					570					575						
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Ser	Ser	Asp	Arg	Cys	Gln	Lys		Val	Gly	Arg	Ser	Val	Ile	Thr	His	
					585						590					
ggt	tat	ggc	agc	act	gca	taa	ttc	tct	tac	tgt	cat	gcc	atc	cgt	aag	7146
Gly	Tyr	Gly	Ser	Thr	Ala		Phe	Ser	Tyr	Cys	His	Ala	Ile	Arg	Lys	
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atg	ctt	ttc	tgt	gac	tgg	tga	gta	ctc	aac	caa	gtc	att	ctg	aga	ata	7194
Met	Leu	Phe	Cys	Asp	Trp		Val	Leu	Asn	Gln	Val	Ile	Leu	Arg	Ile	
					615						620					
gtg	tat	gcg	gcg	acc	gag	ttg	ctc	ttg	ccc	ggc	gtc	aac	acg	gga	taa	7242
Val	Tyr	Ala	Ala	Thr	Glu	Leu	Leu	Leu	Pro	Gly	Val	Asn	Thr	Gly		
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Tyr	Arg	Ala	Thr		Gln	Asn	Phe	Lys	Ser	Ala	His	His	Trp	Lys	Thr	
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ttc	ttc	ggg	gcg	aaa	act	ctc	aag	gat	ctt	acc	gct	ggt	gag	atc	cag	7338
Phe	Phe	Gly	Ala	Lys	Thr	Leu	Lys	Asp	Leu	Thr	Ala	Val	Glu	Ile	Gln	
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Phe	Asp	Val	Thr	His	Ser	Cys	Thr	Gln	Leu	Ile	Phe	Ser	Ile	Phe	Tyr	
				675					680					685		
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Phe	His	Gln	Arg	Phe	Trp	Val	Ser	Lys	Asn	Arg	Lys	Ala	Lys	Cys	Arg	
			690					695					700			
aaa	aaa	ggg	aat	aag	ggc	gac	acg	gaa	atg	ttg	aat	act	cat			7476
Lys	Lys	Gly	Asn	Lys	Gly	Asp	Thr	Glu	Met	Leu	Asn	Thr	His			
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warf Sequence.ST25.txt

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<223> Synthetic Construct

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Ser Ala Ala Leu Ser Ser Asp Gly Arg Ile Phe Thr Gly Val Asn Val
35 40 45

Tyr His Phe Thr Gly Gly Pro Cys Ala Glu Leu Val Val Leu Gly Thr
50 55 60

Ala Ala Ala Ala Ala Ala Gly Asn Leu Thr Cys Ile Val Ala Ile Gly
65 70 75 80

Asn Glu Asn Arg Gly Ile Leu Ser Pro Cys Gly Arg Cys Arg Gln Val
85 90 95

Leu Leu Asp Leu His Pro Gly Ile Lys Ala Ile Val Lys Asp Ser Asp
100 105 110

Gly Gln Pro Thr Ala Val Gly Ile Arg Glu Leu Leu Pro Ser Gly Tyr
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Val Trp Glu Gly
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<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

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Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys Pro
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Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
20 25 30

Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr Leu
35 40 45

warf Sequence.ST25.txt

Thr Cys Glu Thr His Arg Ile Asn Trp Thr Ala Asp Gly Arg Pro Cys
50 55 60

Gly Leu Asn Gly Thr Leu Phe Pro Arg Leu His Val Ser Glu Thr Arg
65 70 75 80

Pro Gln Gly Pro Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
85 90 95

Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
100 105 110

Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
115 120 125

Pro Ile Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
130 135 140

Pro Val Leu Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
145 150 155 160

Leu Leu Pro Ser Phe Asp Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
165 170 175

Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
180 185 190

Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
195 200 205

Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
210 215 220

Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
225 230 235 240

Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
245 250 255

Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
260 265 270

Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
275 280 285

Ile Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp

290

295

Leu Ser Arg Leu Phe
305

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1 5

<210> 18

<211> 75

<212> PRT

<213> Artificial

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<223> Synthetic Construct

<400> 18

Gly Thr Tyr Leu Ser Asp Leu Ser Ile Ser Phe Ile His Ser Cys Leu
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Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr Ile Trp
20 25 30

Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly Ser Arg
35 40 45

Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln Lys Trp
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Ser Cys Asn Phe Ile Arg Leu His Pro Val Tyr
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<210> 19

<211> 5

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

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Leu Leu Pro Gly Ser
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warf Sequence.ST25.txt

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<220>
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<400> 20

Phe Ala Gln Arg Cys Cys His Cys Cys Arg His Arg Gly Val Thr Leu
 1 5 10 15

Val Val Trp Tyr Gly Phe Ile Gln Leu Arg Phe Pro Thr Ile Lys Ala
 20 25 30

Ser Tyr Met Ile Pro His Val Val Gln Lys Ser Gly
 35 40

<210> 21
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<400> 21

Leu Leu Arg Ser Ser Asp Arg Cys Gln Lys
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<220>
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<210> 23
 <211> 15
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 23

Phe Ser Tyr Cys His Ala Ile Arg Lys Met Leu Phe Cys Asp Trp

1 5 15

<210> 24
<211> 24
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 24

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Leu Leu Pro Gly Val Asn Thr Gly
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<210> 25
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<223> Synthetic Construct

<400> 25

Tyr Arg Ala Thr
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<210> 26
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<220>
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<400> 26

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Thr Leu Lys Asp Leu Thr Ala Val Glu Ile Gln Phe Asp Val Thr His
20 25 30

Ser Cys Thr Gln Leu Ile Phe Ser Ile Phe Tyr Phe His Gln Arg Phe
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Trp Val Ser Lys Asn Arg Lys Ala Lys Cys Arg Lys Lys Gly Asn Lys
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Gly Asp Thr Glu Met Leu Asn Thr His
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warf Sequence.ST25.txt

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<223> attB1

<220>
<221> CDS
<222> (3120)..(3590)
<223> trans-dominant BLV Rex (M4)

<220>
<221> misc_feature
<222> (3653)..(4282)
<223> attB2

<220>
<221> misc_signal
<222> (3690)..(4282)
<223> WPRE; woodchuck hepatitis virus post-transcriptional regulatory
      element

<220>
<221> LTR
<222> (4328)..(4921)
<223> 3' MoMuLVLTR

<220>
<221> CDS
<222> (6217)..(7077)
<223> ampicillin resistance

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ggaaaaatac ataactgaga atagaaaagt tcagatcaag gtcaggaaca aagaaacagc      120
tgaataccaa acaggatatc tgttggttaagc ggttcctgcc ccggctcagg gccaagaaca      180
gatgagacag ctgagtgatg ggccaaacag gatatctgtg gtaagcagtt cctgccccgg      240
ctcggggcca agaacagatg gtccccagat gcggtccagc cctcagcagt ttctagttaa      300

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warf Sequence.ST25.txt

tcatcagatg tttccagggt gcccgaagga cctgaaaatg accctgtacc ttatttgaac	360
taaccaatca gttcgtttct cgcttctgtt cgcgcgcttc cgctctccga gctcaataaa	420
agagcccaca acccctcact cggcgcgcca gtcttccgat agactgcgtc gcccgggtac	480
ccgtattccc aataaagcct cttgctgttt gcatccgaat cgtgggtctcg ctgttccttg	540
ggaggggtctc ctctgagtga ttgactaccc acgacggggg tctttcattt ggggggtcgt	600
ccgggatttg gagaccctg cccagggacc accgaccac caccgggagg taagctggcc	660
agcaacttat ctgtgtctgt ccgattgtct agtgtctatg tttgatgtta tgcgcctgcg	720
tctgtactag ttagctaact agctctgtat ctggcgacc cgtggtgga ctgacgagtt	780
ctgaacaccc ggccgcaacc ctgggagacg tcccagggac tttgggggcc gtttttgtgg	840
cccgacctga ggaaggaggt cgatgtggaa tccgaccccg tcaggatatg tggttctggt	900
aggagacgag aacctaaaac agttcccgc tccgtctgaa tttttgcttt cggtttggaa	960
ccgaagccgc gcgtcttgtc tgctgcagcg ctgcagcatc gttctgtgtt gtctctgtct	1020
gactgtgttt ctgtatttgt ctgaaaatta gggccagact gttaccactc ccttaagttt	1080
gaccttaggt cactggaaag atgtcgagcg gatcgctcac aaccagtcgg tagatgtcaa	1140
gaagagacgt tgggttacct tctgctctgc agaattggcca acctttaacg tcggatggcc	1200
gcgagacggc acctttaacc gagacctcat caccaggtt aagatcaagg tcttttcacc	1260
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atccgccccg tctctcccc ttgaacctcc tcgttcgacc ccgcctcgat cctcccttta	1440
tccagccctc actccttctc taggcgccgg aattccgac tgatcaagag acaggatgag	1500
gatcgtttcg c atg att gaa caa gat gga ttg cac gca ggt tct ccg gcc	1550
Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala	
1 5 10	
gct tgg gtg gag agg cta ttc ggc tat gac tgg gca caa cag aca atc	1598
Ala Trp Val Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile	
15 20 25	
ggc tgc tct gat gcc gcc gtg ttc cgg ctg tca gcg cag ggg cgc ccg	1646
Gly Cys Ser Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro	
30 35 40 45	
gtt ctt ttt gtc aag acc gac ctg tcc ggt gcc ctg aat gaa ctg cag	1694
Val Leu Phe Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln	
50 55 60	
gac gag gca gcg cgg cta tcg tgg ctg gcc acg acg ggc gtt cct tgc	1742
Asp Glu Ala Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys	
65 70 75	
gca gct gtg ctc gac gtt gtc act gaa gcg gga agg gac tgg ctg cta	1790
Ala Ala Val Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu	
80 85 90	

warf Sequence.ST25.txt

ttg ggc gaa gtg ccg ggg cag gat ctc ctg tca tct cac ctt gct cct Leu Gly Glu Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro 95 100 105	1838
gcc gag aaa gta tcc atc atg gct gat gca atg cgg cgg ctg cat acg Ala Glu Lys Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr 110 115 120 125	1886
ctt gat ccg gct acc tgc cca ttc gac cac caa gcg aaa cat cgc atc Leu Asp Pro Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile 130 135 140	1934
gag cga gca cgt act cgg atg gaa gcc ggt ctt gtc gat cag gat gat Glu Arg Ala Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp 145 150 155	1982
ctg gac gaa gag cat cag ggg ctc gcg cca gcc gaa ctg ttc gcc agg Leu Asp Glu Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg 160 165 170	2030
ctc aag gcg cgc atg ccc gac ggc gag gat ctc gtc gtg acc cat ggc Leu Lys Ala Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly 175 180 185	2078
gat gcc tgc ttg ccg aat atc atg gtg gaa aat ggc cgc ttt tct gga Asp Ala Cys Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly 190 195 200 205	2126
ttc atc gac tgt ggc cgg ctg ggt gtg gcg gac cgc tat cag gac ata Phe Ile Asp Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile 210 215 220	2174
gcg ttg gct acc cgt gat att gct gaa gag ctt ggc ggc gaa tgg gct Ala Leu Ala Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala 225 230 235	2222
gac cgc ttc ctc gtg ctt tac ggt atc gcc gct ccc gat tcg cag cgc Asp Arg Phe Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg 240 245 250	2270
atc gcc ttc tat cgc ctt ctt gac gag ttc ttc tga gcgggactct Ile Ala Phe Tyr Arg Leu Leu Asp Glu Phe Phe 255 260	2316
gggggttcgaa atgaccgacc aagcgacgcc caacctgccca tcacgagatt tcgattccac	2376
cgccgccttc tatgaaaggt tgggcttcgg aatcgttttc cgggacgccg gctggatgat	2436
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tgattcccc ttaaaattac aactgctaga aaatgaatgg ctctcccgcc ttttttgagg	2736
gggaatcatt tgtatgaaag atcatgccga cctaggcgcc gccaccgccc cgtaaaccag	2796
acagagacgt cagctgccag aaaagctggt gacggcagct ggtggctaga atccccgtac	2856

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aaaagcaggc	ttcgaaggag	atagaaccaa	ttctctaagg	aaataacttaa	cgtcgactgg	3096							
atccggtacc	gaattcgatc	cac	atg	cct	aaa	aaa	cga	cgg	tcc	cga	aga	cgc	3149
			Met	Pro	Lys	Lys	Arg	Arg	Ser	Arg	Arg	Arg	
			265					270					

ctc	tac	atg	cct	gcc	cgg	ccc	tgg	ttt	tgt	cca	atg	atg	tca	cca	tcg	3245
Leu	Tyr	Met	Pro	Ala	Arg	Pro	Trp	Phe	Cys	Pro	Met	Met	Ser	Pro	Ser	
				295					300					305		

gga tgc aca cca cgc tca cct gcg aga ccc acc gta tca act gga ccg 3341
Gly Ser Thr Pro Arg Ser Pro Ala Arg Pro Thr Val Ser Thr Gly Pro
325 330 335

atg tct ccg aga ccc gcc ccc aag ggc ccc gac gac tct gga tca act 3437
Met Ser Pro Arg Pro Ala Pro Lys Gly Pro Asp Asp Ser Gly Ser Thr
355 360 365 370

cct tcg agc ggt ccc cct tcc agc cct acc aat gcc aat tgc cct cgg 3533
Pro Ser Ser Gly Pro Pro Ser Ser Pro Thr Asn Ala Asn Cys Pro Arg

aca act tag taacgcatcc tgtcctcaga aaagtcctta tattaaatca 3630
Thr Thr
420

aaatcaacgtc tggattacaa aattttgtgaa agattgactg gtattcttaa ctatgttgct 3750

ccttttacgc tatgtggata cgctgcttta atgcctttgt atcatgctat tgcttcccgt 3810

tggcccgattg tcaggcaacg tggcgtggtg tgcactgtgt ttgctgacgc aacccccact 3930

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Warf Sequence.ST25.txt

attgccacgg	cggaactcat	cgccgcctgc	cttgcgccgt	gctggacagg	ggctcggctg	4050
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Warf Sequence.ST25.txt

tgctacagag ttcttgaagt ggtggcctaa ctacggctac actagaagga cagtatttgg	5910
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cgaaaactca cgtaagggga ttttgggtcat gagattatca aaaaggatct tcacctagat	6150
ccttttaaat taaaaatgaa gttttaaatc aatctaaagt atatatgagt aaacttggtc	6210
tgacag tta cca atg ctt aat cag tga ggc acc tat ctc agc gat ctg Leu Pro Met Leu Asn Gln Gly Thr Tyr Leu Ser Asp Leu	6258
	425 430
tct att tcg ttc atc cat agt tgc ctg act ccc cgt cgt gta gat aac Ser Ile Ser Phe Ile His Ser Cys Leu Thr Pro Arg Arg Val Asp Asn	6306
	435 440 445
tac gat acg gga ggg ctt acc atc tgg ccc cag tgc tgc aat gat acc Tyr Asp Thr Gly Gly Leu Thr Ile Trp Pro Gln Cys Cys Asn Asp Thr	6354
	450 455 460 465
gcg aga ccc acg ctc acc ggc tcc aga ttt atc agc aat aaa cca gcc Ala Arg Pro Thr Leu Thr Gly Ser Arg Phe Ile Ser Asn Lys Pro Ala	6402
	470 475 480
agc cgg aag ggc cga gcg cag aag tgg tcc tgc aac ttt atc cgc ctc Ser Arg Lys Gly Arg Ala Gln Lys Trp Ser Cys Asn Phe Ile Arg Leu	6450
	485 490 495
cat cca gtc tat taa ttg ttg ccg gga agc tag agt aag tag ttc gcc His Pro Val Tyr Leu Leu Pro Gly Ser Ser Lys Phe Ala	6498
	500 505 510
agt taa tag ttt gcg caa cgt tgt tgc cat tgc tgc agg cat cgt ggt Ser Phe Ala Gln Arg Cys Cys His Cys Cys Arg His Arg Gly	6546
	515 520
gtc acg ctc gtc gtt tgg tat ggc ttc att cag ctc cgg ttc cca acg Val Thr Leu Val Val Trp Tyr Gly Phe Ile Gln Leu Arg Phe Pro Thr	6594
	525 530 535 540
atc aag gcg agt tac atg atc ccc cat gtt gtg caa aaa agc ggt tag Ile Lys Ala Ser Tyr Met Ile Pro His Val Val Gln Lys Ser Gly	6642
	545 550 555
ctc ctt cgg tcc tcc gat cgt tgt cag aag taa gtt ggc cgc agt gtt Leu Leu Arg Ser Ser Asp Arg Cys Gln Lys Val Val Gly Arg Ser Val	6690
	560 565 570
atc act cat ggt tat ggc agc act gca taa ttc tct tac tgt cat gcc Ile Thr His Gly Tyr Gly Ser Thr Ala Phe Ser Tyr Cys His Ala	6738
	575 580 585
atc cgt aag atg ctt ttc tgt gac tgg tga gta ctc aac caa gtc att Ile Arg Lys Met Leu Phe Cys Asp Trp Val Leu Asn Gln Val Ile	6786
	590 595 600
ctg aga ata gtg tat gcg gcg acc gag ttg ctc ttg ccc ggc gtc aac Leu Arg Ile Val Tyr Ala Ala Thr Glu Leu Leu Leu Pro Gly Val Asn	6834
	605 610 615

warf Sequence.ST25.txt

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acg gga taa tac cgc gcc aca tag cag aac ttt aaa agt gct cat cat 6882
Thr Gly Tyr Arg Ala Thr Gln Asn Phe Lys Ser Ala His His 630
620 625

tgg aaa acg ttc ttc ggg gcg aaa act ctc aag gat ctt acc gct gtt 6930
Trp Lys Thr Phe Phe Gly Ala Lys Thr Leu Lys Asp Leu Thr Ala Val 645
635 640

gag atc cag ttc gat gta acc cac tcg tgc acc caa ctg atc ttc agc 6978
Glu Ile Gln Phe Asp Val Thr His Ser Cys Thr Gln Leu Ile Phe Ser 660
650 655

atc ttt tac ttt cac cag cgt ttc tgg gtg agc aaa aac agg aag gca 7026
Ile Phe Tyr Phe His Gln Arg Phe Trp Val Ser Lys Asn Arg Lys Ala 675
665 670

aaa tgc cgc aaa aaa ggg aat aag ggc gac acg gaa atg ttg aat act 7074
Lys Cys Arg Lys Lys Gly Asn Lys Gly Asp Thr Glu Met Leu Asn Thr 690
680 685

cat actcttcctt tttcaatatt attgaagcat ttatcagggt tattgtctca 7127
His 695

tgagcggata catatttgaa tgtatttaga aaaataaaca aataggggtt ccgcgcacat 7187

ttccccgaaa agtgccacct gacgtctaag aaaccattat tatcatgaca ttaacctata 7247

aaaataggcg tatcacgagg ccttttcgtc ttcaagaatt aattcatacc agatcaccga 7307

aaactgtcct ccaaattgtgt ccccttcaca ctcccaaatt cgcgggcttc tgcctcttag 7367

accactctac cctattcccc acactcacg gagccaaagc cgcgggccctt ccgtttcttt 7427

gct 7430

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<210> 28
 <211> 264
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 28

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Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
1      5      10      15

```

```

Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
20      25      30

```

```

Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
35      40      45

```

```

Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
50      55      60

```

warf Sequence.ST25.txt

Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65 70 75 80

Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
85 90 95

Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
100 105 110

Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
115 120 125

Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
130 135 140

Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145 150 155 160

Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
165 170 175

Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
180 185 190

Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
195 200 205

Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
210 215 220

Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225 230 235 240

Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
245 250 255

Tyr Arg Leu Leu Asp Glu Phe Phe
260

<210> 29
<211> 156
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 29

Warf Sequence.ST25.txt

Met Pro Lys Lys Arg Arg Ser Arg Arg Arg Pro Gln Pro Ile Ile Arg
1 5 10 15

Trp Gln Val Leu Leu Val Gly Gly Pro Thr Leu Tyr Met Pro Ala Arg
20 25 30

Pro Trp Phe Cys Pro Met Met Ser Pro Ser Met Pro Gly Ala Pro Ser
35 40 45

Ala Gly Pro Met Ser Asp Ser Asn Ser Lys Gly Ser Thr Pro Arg Ser
50 55 60

Pro Ala Arg Pro Thr Val Ser Thr Gly Pro Pro Met Asp Asp Leu Ala
65 70 75 80

Ala Ser Met Glu Arg Cys Ser Leu Asp Cys Met Ser Pro Arg Pro Ala
85 90 95

Pro Lys Gly Pro Asp Asp Ser Gly Ser Thr Ala Pro Phe Arg Pro Phe
100 105 110

Ala Leu Ser Pro Ala Arg Leu Asp Leu Pro Pro Ser Ser Gly Pro Pro
115 120 125

Ser Ser Pro Thr Asn Ala Asn Cys Pro Arg Pro Leu Ala Thr Val Ala
130 135 140

Pro Leu Ser Gly Thr Ala Phe Phe Pro Gly Thr Thr
145 150 155

<210> 30
<211> 6
<212> PRT
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<220>
<223> Synthetic Construct

<400> 30

Leu Pro Met Leu Asn Gln
1 5

<210> 31
<211> 75
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 31

warf Sequence.ST25.txt

Gly Thr Tyr Leu Ser Asp Leu Ser Ile Ser Phe Ile His Ser Cys Leu
1 5 10 15

Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr Ile Trp
20 25 30

Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly Ser Arg
35 40 45

Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln Lys Trp
50 55 60

Ser Cys Asn Phe Ile Arg Leu His Pro Val Tyr
65 70 75

<210> 32
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 32

Leu Leu Pro Gly Ser
1 5

<210> 33
<211> 44
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 33

Phe Ala Gln Arg Cys Cys His Cys Cys Arg His Arg Gly Val Thr Leu
1 5 10 15

Val Val Trp Tyr Gly Phe Ile Gln Leu Arg Phe Pro Thr Ile Lys Ala
20 25 30

Ser Tyr Met Ile Pro His Val Val Gln Lys Ser Gly
35 40

<210> 34
<211> 10
<212> PRT
<213> Artificial

<220>

<223> Synthetic Construct

<400> 34

Leu Leu Arg Ser Ser Asp Arg Cys Gln Lys
1 5 10

<210> 35

<211> 14

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 35

Val Gly Arg Ser Val Ile Thr His Gly Tyr Gly Ser Thr Ala
1 5 10

<210> 36

<211> 15

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 36

Phe Ser Tyr Cys His Ala Ile Arg Lys Met Leu Phe Cys Asp Trp
1 5 10 15

<210> 37

<211> 24

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 37

Val Leu Asn Gln Val Ile Leu Arg Ile Val Tyr Ala Ala Thr Glu Leu
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Leu Leu Pro Gly Val Asn Thr Gly
20

<210> 38

<211> 4

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 38

warf Sequence.ST25.txt

Tyr Arg Ala Thr
1

<210> 39
<211> 73
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 39

Gln Asn Phe Lys Ser Ala His His Trp Lys Thr Phe Phe Gly Ala Lys
1 5 10 15

Thr Leu Lys Asp Leu Thr Ala Val Glu Ile Gln Phe Asp Val Thr His
20 25 30

Ser Cys Thr Gln Leu Ile Phe Ser Ile Phe Tyr Phe His Gln Arg Phe
35 40 45

Trp Val Ser Lys Asn Arg Lys Ala Lys Cys Arg Lys Lys Gly Asn Lys
50 55 60

Gly Asp Thr Glu Met Leu Asn Thr His
65 70

<210> 40
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<212> DNA
<213> Artificial

<220>
<223> Engineered Sequence from virus and plasmid

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<222> (149)..(737)
<223> 5' MoMuSVLTR

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<222> (1660)..(2454)
<223> neomycin resistance

<220>
<221> promoter
<222> (2806)..(3150)
<223> BLV promoter

<220>
<221> misc_feature
<222> (3170)..(3194)
<223> attb1

warf Sequence.ST25.txt

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 <221> CDS
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 <223> EYFP; enhanced yellow florescent protein

<220>
 <221> misc_feature
 <222> (3980)..(4004)
 <223> attb2

<220>
 <221> LTR
 <222> (4056)..(4649)
 <223> 3' MoMuSVLTR

<220>
 <221> CDS
 <222> (5945)..(6805)
 <223> ampicillin resistance

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aaagccgcgg cccttcggtt tctttgcttt tgaaagaccc caccgtagg  tggcaagcta      180
gcttaagtaa cgccactttg caaggcatgg aaaaatacat aactgagaat agaaaagttc      240
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tatctgtggt aagcagttcc tgccccggct cggggccaag aacagatggt ccccagatgc      420
ggtccagccc tcagcagttt ctagtgaatc atcagatggt tccagggcgc cccaaggacc      480
tgaaaatgac cctgtacctt atttgaacta accaatcagt tcgcttctcg cttctgttcg      540
cgcgcttccg ctctccgagc tcaataaaag agcccacaac ccctcactcg gcgcgccagt      600
cttccgatag actgcgtcgc ccgggtaccc gtattcccaa taaagcctct tgctgtttgc      660
atccgaatcg tggctctcgt gttccttggg agggctctct ctgagtgatt gactaccac      720
gacggggggtc tttcatttgg gggctcgtcc gggatttggg gacccttgc cagggaccac      780
cgaccaccca ccgggaggta agctggccag caacttatct gtgtctgtcc gattgtctag      840
tgtctatggt tgatgttatg cgctgcgtc tgtactagtt agctaactag ctctgtatct      900
ggcggacccg tgggtggaact gacgagttct gaacaccg cgcgaaccct gggagacgtc      960
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gccagactgt taccactccc ttaagtttga ccttaggtca ctggaaagat gtcgagcgga     1260
    
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warf Sequence.ST25.txt

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gttcgacccc gcctcgatcc tccctttatc cagccctcac tcctttctcta ggcgccggaa	1620
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	Met Ile Glu Gln Asp 1 5
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Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val Glu Arg Leu Phe Gly	10 15 20
tat gac tgg gca caa cag aca atc ggc tgc tct gat gcc gcc gtg ttc	1770
Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser Asp Ala Ala Val Phe	25 30 35
cggtctg tca gcg cag ggg cgc ccg gtt ctt ttt gtc aag acc gac ctg	1818
Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe Val Lys Thr Asp Leu	40 45 50
tcc ggt gcc ctg aat gaa ctg cag gac gag gca gcg cgg cta tcg tgg	1866
Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala Ala Arg Leu Ser Trp	55 60 65
ctg gcc acg acg ggc gtt cct tgc gca gct gtg ctc gac gtt gtc act	1914
Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val Leu Asp Val Val Thr	70 75 80 85
gaa gcg gga agg gac tgg ctg cta ttg ggc gaa gtg ccg ggg cag gat	1962
Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu Val Pro Gly Gln Asp	90 95 100
ctc ctg tca tct cac ctt gct cct gcc gag aaa gta tcc atc atg gct	2010
Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys Val Ser Ile Met Ala	105 110 115
gat gca atg ccg ccg ctg cat acg ctt gat ccg gct acc tgc cca ttc	2058
Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro Ala Thr Cys Pro Phe	120 125 130
gac cac caa gcg aaa cat cgc atc gag cga gca cgt act cgg atg gaa	2106
Asp His Gln Ala Lys His Arg Ile Glu Arg Ala Arg Thr Arg Met Glu	135 140 145
gcc ggt ctt gtc gat cag gat gat ctg gac gaa gag cat cag ggg ctc	2154
Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu Glu His Gln Gly Leu	150 155 160 165
gcg cca gcc gaa ctg ttc gcc agg ctc aag gcg cgc atg ccc gac ggc	2202
Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala Arg Met Pro Asp Gly	170 175 180
gag gat ctc gtc gtg acc cat ggc gat gcc tgc ttg ccg aat atc atg	2250
Glu Asp Leu Val Val Thr His Gly Asp Ala Cys Leu Pro Asn Ile Met	

Warf Sequence.ST25.txt

185	190	195	
gtg gaa aat ggc cgc ttt tct gga ttc atc gac tgt ggc cgg ctg ggt Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp Cys Gly Arg Leu Gly 200 205 210			2298
gtg gcg gac cgc tat cag gac ata gcg ttg gct acc cgt gat att gct Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala Thr Arg Asp Ile Ala 215 220 225			2346
gaa gag ctt ggc ggc gaa tgg gct gac cgc ttc ctc gtg ctt tac ggt Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe Leu Val Leu Tyr Gly 230 235 240 245			2394
atc gcc gct ccc gat tcg cag cgc atc gcc ttc tat cgc ctt ctt gac Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe Tyr Arg Leu Leu Asp 250 255 260			2442
gag ttc ttc tga gcgggactct ggggttcgaa atgaccgacc aagcgacgcc Glu Phe Phe			2494
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ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta aac ggc cac Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His 275 280 285 290			3313
aag ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc tac ggc aag Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys 295 300 305			3361
ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp 310 315 320			3409
ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc gcc cgc			3457

Warf Sequence.ST25.txt

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tac	ccc	gac	cac	atg	aag	cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	3505
Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	
	340					345					350					
gaa	ggc	tac	gtc	cag	gag	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	3553
Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	
355					360					365					370	
tac	aag	acc	cgc	gcc	gag	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	3601
Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	
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cgc	atc	gag	ctg	aag	ggc	atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	3649
Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	
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ggg	cac	aag	ctg	gag	tac	aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	3697
Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	
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gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	3745
Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	
	420					425					430					
aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	3793
Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	
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acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	3841
Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	
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agc	tac	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	3889
Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	
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atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	3937
Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	
		485					490					495				
gac	gag	ctg	tac	aag	taa	agc	ggccgca	ctc	gagatat	ctagacccag						3985
Asp	Glu	Leu	Tyr	Lys												
	500															
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warf Sequence.ST25.txt

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                                Leu Pro Met Leu Asn
                                505

cag tga ggc acc tat ctc agc gat ctg tct att tcg ttc atc cat agt 6007
Gln   Gly Thr Tyr Leu Ser Asp Leu Ser Ile Ser Phe Ile His Ser
      510                                515                                520

tgc ctg act ccc cgt cgt gta gat aac tac gat acg gga ggg ctt acc 6055
Cys Leu Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr
      525                                530                                535

atc tgg ccc cag tgc tgc aat gat acc gcg aga ccc acg ctc acc ggc 6103
Ile Trp Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly
540                                545                                550                                555

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warf Sequence.ST25.txt

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aag tgg tcc tgc aac ttt atc cgc ctc cat cca gtc tat taa ttg ttg Lys Trp Ser Cys Asn Phe Ile Arg Leu His Pro Val Tyr Leu Leu 575 580 585	6199
ccg gga agc tag agt aag tag ttc gcc agt taa tag ttt gcg caa cgt Pro Gly Ser Ser Lys Phe Ala Ser Phe Ala Gln Arg 590 595	6247
tgt tgc cat tgc tgc agg cat cgt ggt gtc acg ctc gtc gtt tgg tat Cys Cys His Cys Cys Arg His Arg Gly Val Thr Leu Val Val Trp Tyr 600 605 610	6295
ggc ttc att cag ctc cgg ttc cca acg atc aag gcg agt tac atg atc Gly Phe Ile Gln Leu Arg Phe Pro Thr Ile Lys Ala Ser Tyr Met Ile 615 620 630	6343
ccc cat gtt gtg caa aaa agc ggt tag ctc ctt cgg tcc tcc gat cgt Pro His Val Val Gln Lys Ser Gly Leu Leu Arg Ser Ser Asp Arg 635 640 645	6391
tgt cag aag taa gtt ggc cgc agt gtt atc act cat ggt tat ggc agc Cys Gln Lys Val Gly Arg Ser Val Ile Thr His Gly Tyr Gly Ser 650 655 660	6439
act gca taa ttc tct tac tgt cat gcc atc cgt aag atg ctt ttc tgt Thr Ala Phe Ser Tyr Cys His Ala Ile Arg Lys Met Leu Phe Cys 665 670 675	6487
gac tgg tga gta ctc aac caa gtc att ctg aga ata gtg tat gcg gcg Asp Trp Val Leu Asn Gln Val Ile Leu Arg Ile Val Tyr Ala Ala 680 685 690	6535
acc gag ttg ctc ttg ccc ggc gtc aac acg gga taa tac cgc gcc aca Thr Glu Leu Leu Leu Pro Gly Val Asn Thr Gly Tyr Arg Ala Thr 695 700 705	6583
tag cag aac ttt aaa agt gct cat cat tgg aaa acg ttc ttc ggg gcg Gln Asn Phe Lys Ser Ala His His Trp Lys Thr Phe Phe Gly Ala 710 715 720	6631
aaa act ctc aag gat ctt acc gct gtt gag atc cag ttc gat gta acc Lys Thr Leu Lys Asp Leu Thr Ala Val Glu Ile Gln Phe Asp Val Thr 725 730 735	6679
cac tcg tgc acc caa ctg atc ttc agc atc ttt tac ttt cac cag cgt His Ser Cys Thr Gln Leu Ile Phe Ser Ile Phe Tyr Phe His Gln Arg 740 745 750	6727
ttc tgg gtg agc aaa aac agg aag gca aaa tgc cgc aaa aaa ggg aat Phe Trp Val Ser Lys Asn Arg Lys Ala Lys Cys Arg Lys Lys Gly Asn 755 760 765	6775
aag ggc gac acg gaa atg ttg aat act cat actcttcctt tttcaatatt Lys Gly Asp Thr Glu Met Leu Asn Thr His	6825
attgaagcat ttatcagggt tattgtctca tgagcggata catatttgaa tgtatttaga	6885

Warf Sequence.ST25.txt

aaaataaaca aataggggtt ccgcgcacat ttccccgaaa agtgccacct gacgtctaag 6945
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 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 41

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Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
 20 25 30

Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
 35 40 45

Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
 50 55 60

Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
 65 70 75 80

Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
 85 90 95

Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
 100 105 110

Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
 115 120 125

Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
 130 135 140

Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
 145 150 155 160

Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
 165 170 175

Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
 180 185 190

warf Sequence.ST25.txt

Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
195 200 205

Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
210 215 220

Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225 230 235 240

Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
245 250 255

Tyr Arg Leu Leu Asp Glu Phe Phe
260

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<211> 239
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 42

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

warf Sequence.ST25.txt

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 43
<211> 6
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 43

Leu Pro Met Leu Asn Gln
1 5

<210> 44
<211> 75
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 44

Gly Thr Tyr Leu Ser Asp Leu Ser Ile Ser Phe Ile His Ser Cys Leu
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Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr Ile Trp
20 25 30

Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly Ser Arg
35 40 45

warf Sequence.ST25.txt

Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln Lys Trp
50 55 60

Ser Cys Asn Phe Ile Arg Leu His Pro Val Tyr
65 70 75

<210> 45
<211> 5
<212> PRT
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<220>
<223> Synthetic Construct

<400> 45

Leu Leu Pro Gly Ser
1 5

<210> 46
<211> 44
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 46

Phe Ala Gln Arg Cys Cys His Cys Cys Arg His Arg Gly Val Thr Leu
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Val Val Trp Tyr Gly Phe Ile Gln Leu Arg Phe Pro Thr Ile Lys Ala
20 25 30

Ser Tyr Met Ile Pro His Val Val Gln Lys Ser Gly
35 40

<210> 47
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<400> 47

Leu Leu Arg Ser Ser Asp Arg Cys Gln Lys
1 5 10

<210> 48
<211> 14
<212> PRT

warf Sequence.ST25.txt

<213> Artificial

<220>

<223> Synthetic Construct

<400> 48

Val Gly Arg Ser Val Ile Thr His Gly Tyr Gly Ser Thr Ala
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<210> 49

<211> 15

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<400> 49

Phe Ser Tyr Cys His Ala Ile Arg Lys Met Leu Phe Cys Asp Trp
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<211> 24

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<213> Artificial

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<223> Synthetic Construct

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1 5 10 15

Leu Leu Pro Gly Val Asn Thr Gly
20

<210> 51

<211> 4

<212> PRT

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<223> Synthetic Construct

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<211> 73

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<213> Artificial

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warf Sequence.ST25.txt

<223> Synthetic Construct

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Ser Cys Thr Gln Leu Ile Phe Ser Ile Phe Tyr Phe His Gln Arg Phe
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Gly Asp Thr Glu Met Leu Asn Thr His
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<211> 7121

<212> DNA

<213> Artificial

<220>

<223> Engineered Sequence from virus and plasmid

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<223> 5' MoMuSVLTR

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<221> CDS

<222> (1660)..(2454)

<223> neomycin resistance

<220>

<221> promoter

<222> (2806)..(3261)

<223> HIV promoter

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<221> misc_feature

<222> (3281)..(3305)

<223> attB1

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<222> (3347)..(4066)

<223> EYFP; enhanced yellow florescent protein

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<221> misc_feature

<222> (4091)..(4115)

<223> attB2

warf Sequence.ST25.txt

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cgaccccgtc aggatatgtg gttctggtag gagacgagaa cctaaaacag ttcccgcctc     1080
cgtctgaatt tttgctttcg gtttggaacc gaagccgcgc gtcttgtctg ctgcagcgt      1140
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Warf Sequence.ST25.txt

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gga ttg cac gca ggt tct ccg gcc gct tgg gtg gag agg cta ttc ggc Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val Glu Arg Leu Phe Gly 10 15 20	1722
tat gac tgg gca caa cag aca atc ggc tgc tct gat gcc gcc gtg ttc Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser Asp Ala Ala Val Phe 25 30 35	1770
cgg ctg tca gcg cag ggg cgc ccg gtt ctt ttt gtc aag acc gac ctg Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe Val Lys Thr Asp Leu 40 45 50	1818
tcc ggt gcc ctg aat gaa ctg cag gac gag gca gcg cgg cta tcg tgg Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala Ala Arg Leu Ser Trp 55 60 65	1866
ctg gcc acg acg ggc gtt cct tgc gca gct gtg ctc gac gtt gtc act Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val Leu Asp Val Val Thr 70 75 80 85	1914
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ctc ctg tca tct cac ctt gct cct gcc gag aaa gta tcc atc atg gct Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys Val Ser Ile Met Ala 105 110 115	2010
gat gca atg cgg cgg ctg cat acg ctt gat ccg gct acc tgc cca ttc Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro Ala Thr Cys Pro Phe 120 125 130	2058
gac cac caa gcg aaa cat cgc atc gag cga gca cgt act cgg atg gaa Asp His Gln Ala Lys His Arg Ile Glu Arg Ala Arg Thr Arg Met Glu 135 140 145	2106
gcc ggt ctt gtc gat cag gat gat ctg gac gaa gag cat cag ggg ctc Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu Glu His Gln Gly Leu 150 155 160 165	2154
gcg cca gcc gaa ctg ttc gcc agg ctc aag gcg cgc atg ccc gac ggc Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala Arg Met Pro Asp Gly 170 175 180	2202
gag gat ctc gtc gtg acc cat ggc gat gcc tgc ttg ccg aat atc atg Glu Asp Leu Val Val Thr His Gly Asp Ala Cys Leu Pro Asn Ile Met 185 190 195	2250
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gtg gcg gac cgc tat cag gac ata gcg ttg gct acc cgt gat att gct Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala Thr Arg Asp Ile Ala 215 220 225	2346
gaa gag ctt ggc ggc gaa tgg gct gac cgc ttc ctc gtg ctt tac ggt	2394

Warf Sequence.ST25.txt

Glu	Glu	Leu	Gly	Gly	Glu	Trp	Ala	Asp	Arg	Phe	Leu	Val	Leu	Tyr	Gly		
230					235					240					245		
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Ile	Ala	Ala	Pro	Asp	Ser	Gln	Arg	Ile	Ala	Phe	Tyr	Arg	Leu	Leu	Asp		
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gag	ttc	ttc	tga	gcgggactct	gggggttcgaa	atgaccgacc	aagcgacgcc										2494
Glu	Phe	Phe															
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ccc	atc	ctg	gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc		3433
Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser		
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gtg	tcc	ggc	gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg		3481
Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu		
	295					300					305						
aag	ttc	atc	tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc		3529
Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu		
310					315					320					325		
gtg	acc	acc	ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac		3577
Val	Thr	Thr	Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp		
				330					335					340			
cac	atg	aag	cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac		3625
His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr		
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Warf Sequence.ST25.txt

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cgc gcc gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu 375 380 385	3721
ctg aag ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys 390 395 400 405	3769
ctg gag tac aac tac aac agc cac aac gtc tat atc atg gcc gac aag Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys 410 415 420	3817
cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu 425 430 435	3865
gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile 440 445 450	3913
ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln 455 460 465	3961
tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu 470 475 480 485	4009
ctg gag ttc gtg acc gcc gcc ggc atc act ctc ggc atg gac gag ctg Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu 490 495 500	4057
tac aag taa agcggccgca ctcgagatat ctagaccag ctttcttgta Tyr Lys	4106
caaagtgggtg ataacatcga taaaataaaa gattttatatt agtctccaga aaaagggggg	4166
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warf Sequence.ST25.txt

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	Leu Pro Met Leu Asn Gln Gly 505 510
acc tat ctg agc gat ctg tct att tcg ttc atc cat agt tgc ctg act	6127
Thr Tyr Leu Ser Asp Leu Ser Ile Ser Phe Ile His Ser Cys Leu Thr	515 520 525
ccc cgt cgt gta gat aac tac gat acg gga ggg ctt acc atc tgg ccc	6175
Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr Ile Trp Pro	530 535 540
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Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly Ser Arg Phe	545 550 555
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Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln Lys Trp Ser	560 565 570
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Cys Asn Phe Ile Arg Leu His Pro Val Tyr Leu Leu Pro Gly Ser	

warf Sequence.ST25.txt
585

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Cys	Cys	Arg	His	Arg	Gly	Val	Thr	Leu	Val	Val	Trp	Tyr	Gly	Phe	Ile			
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Gln	Leu	Arg	Phe	Pro	Thr	Ile	Lys	Ala	Ser	Tyr	Met	Ile	Pro	His	Val			
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Leu	Leu	Pro	Gly	Val	Asn	Thr	Gly		Tyr	Arg	Ala	Thr		Gln	Asn			
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Lys	Asp	Leu	Thr	Ala	Val	Glu	Ile	Gln	Phe	Asp	Val	Thr	His	Ser	Cys			
	725					730					735							
acc	caa	ctg	atc	ttc	agc	atc	ttt	tac	ttt	cac	cag	cgt	ttc	tgg	gtg			6847
Thr	Gln	Leu	Ile	Phe	Ser	Ile	Phe	Tyr	Phe	His	Gln	Arg	Phe	Trp	Val			
	740					745				750					755			
agc	aaa	aac	agg	aag	gca	aaa	tgc	cgc	aaa	aaa	ggg	aat	aag	ggc	gac			6895
Ser	Lys	Asn	Arg	Lys	Ala	Lys	Cys	Arg	Lys	Lys	Gly	Asn	Lys	Gly	Asp			
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acg	gaa	atg	ttg	aat	act	cat	actcttcctt	tttcaatatt	attgaagcat									6946
Thr	Glu	Met	Leu	Asn	Thr	His												
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Warf Sequence.ST25.txt

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<400> 54

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Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
35     40     45

Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
50     55     60

Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65     70     75     80

Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
85     90     95

Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
100    105    110

Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
115    120    125

Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
130    135    140

Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145    150    155    160

Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
165    170    175

Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
180    185    190

Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
195    200    205

Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
210    215    220

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Warf Sequence.ST25.txt

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Tyr Arg Leu Leu Asp Glu Phe Phe
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

warf Sequence.ST25.txt

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

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Leu Pro Met Leu Asn Gln
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Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr Ile Trp
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Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly Ser Arg
35 40 45

Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln Lys Trp
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Ser Cys Asn Phe Ile Arg Leu His Pro Val Tyr
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warf Sequence.ST25.txt

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Val Val Trp Tyr Gly Phe Ile Gln Leu Arg Phe Pro Thr Ile Lys Ala
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Ser Tyr Met Ile Pro His Val Val Gln Lys Ser Gly
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Val Gly Arg Ser Val Ile Thr His Gly Tyr Gly Ser Thr Ala
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warf Sequence.ST25.txt

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Leu Leu Pro Gly Val Asn Thr Gly
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Tyr Arg Ala Thr
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Gln Asn Phe Lys Ser Ala His His Trp Lys Thr Phe Phe Gly Ala Lys
 1 5 10 15

Thr Leu Lys Asp Leu Thr Ala Val Glu Ile Gln Phe Asp Val Thr His
 Page 58

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Ser Cys Thr Gln Leu Ile Phe Ser Ile Phe Tyr Phe His Gln Arg Phe
35 40 45

Trp Val Ser Lys Asn Arg Lys Ala Lys Cys Arg Lys Lys Gly Asn Lys
50 55 60

Gly Asp Thr Glu Met Leu Asn Thr His
65 70